

Result No.	Query	Score	Match	Length	DB	ID	Description
1	799.5	48.3	286	1	MIND_MESVI	Q9mum5	mesostigma
2	792	47.9	282	1	MIND_CHLVU	P56346	chlorella v
3	694.5	42.0	269	1	MIND_GUITH	O78436	guillardia
4	643	38.9	266	1	MIND_SYNY3	Q55900	synecocyst
5	523	31.6	268	1	MIND_BACSU	Q01464	bacillus su
6	506.5	30.6	268	1	MIND_HELPY	Q25098	helicobacte
7	500.5	30.3	268	1	MIND_HELPY	Q9zma8	helicobacte
8	479	29.0	269	1	MIND_ECOLI	P18197	escherichia
9	475.5	28.7	271	1	MIND_THEMEA	Q9x2i3	thermotoga
10	460	27.8	269	1	MIND_BUCAI	P57411	buchnera ap
11	300	18.1	264	1	Y547_METJA	Q57967	methanococc
12	242	14.6	263	1	Y169_METJA	Q57633	methanococc
13	214	12.9	298	1	YLX8_BACSU	P40742	bacillus su
14	213	12.9	353	1	MRP_SYNY3	P53383	synecocyst
15	211	12.8	364	1	MRP_AQUAE	O66946	aquifex ae
16	209	12.6	368	1	MRP_HELPY	Q9zmm5	helicobacte
17	206	12.5	368	1	MRP_HELPY	O24999	helicobacte
18	197.5	11.9	350	1	MRP_DEIRA	Q9rmv9	deinococcus
19	193.5	11.7	295	1	Y949_PYRHO	O58667	pyrococcus
20	191	11.5	290	1	Y283_METJA	Q57731	methanococ
21	190	11.5	381	1	MRP_MYCTU	O33225	mycobacteri
22	183.5	11.1	253	1	Y685_METJA	Q58098	methanococc
23	183	11.1	253	1	SOJ_BACSU	P37522	bacillus su
24	181	10.9	287	1	YCAB_PSEFR	P72190	pseudomonas
25	177.5	10.7	383	1	MRP_MYCLE	P53382	mycobacteri
26	173.5	10.5	271	1	NUB2_HUMAN	Q9V5Y2	homo sapien
27	173.5	10.5	369	1	MRP_ECOLI	P21590	escherichia
28	165	10.0	257	1	Y823_METJA	Q58233	methanococ
29	164.5	9.9	267	1	PABA_CAUCR	O05189	caulobacter
30	164.5	9.9	275	1	NUB2_MOUSE	Q9R061	mus musculus
31	161	9.7	263	1	Y924_METJA	Q58334	methanococc
32	160.5	9.7	287	1	BCHL_HELMO	Q9zgf0	heliobacill
33	153.5	9.3	290	1	BCHL_RHORI	Q91815	rhodospiril

QY 165 DALKTRPEGSPDFIIIDCPAGIDAGF

Db 122 DSTRLR---NVNFTLIDCPAGIDVCFVNAVAPAEAVVUTTPETITSIRDADRACGLLEAS 178
QY 225 GIRDIKIVNVRVDMKINGEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 284
Db 179 GIVEKLVNVRVDMKINGEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 238
QY 285 PPTLAGLAFEOAARWLFEODSMKAVMVEEPPKRG 319
Db 239 KLLUGSISFENAAARLV---GRKEYLVNLTGNGK 270

RESULT 2

MIND_CHLVU STANDARD: PRT: 282 AA.
AC P36346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Chlorella vulgaris.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales.
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IAM C-27 / TAMIYA;
RC MEDLINE=97303241; PubMed=9159184;
RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugitani M.,
RT "Complete nucleotide sequence of the chloroplast genome from the
RT green alga Chlorella vulgaris: the existence of genes possibly
RT involved in chloroplast division."
RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997)
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC
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CC Or send an email to license@isb-sib.ch).
CC
CC EMBL: AB001684; BAA57051.1;
DR InterPro: IPR000707; Para.
DR Pfam: PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Chloroplast.
FT NP_BIND 24 31 ATP (POTENTIAL).
SQ SEQUENCE 282 AA: 31013 MW: 94010DDA5A6AEC7 CRC64;

Query Match 47.9%; Score 792; DB 1; Length 282;
Best Local Similarity 60.4%; Pred. No. 7.4e-57;
Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

QY 59 RIVVITSGKGGVCKTTTANVGLSLARYGSVVAIDAGLRLNLDLLGLNVRVNTQVE 118
Db 17 RVVITSGKGGVCKTTTANVGLSLARYGSVVAIDAGLRLNLDLLGLNVRVNTQVE 76
QY 119 VINGCDRLDQALVRKRWNSFELLCSKPSKLPMPGFGGKALEWLVDAKTRPESPDFI 178
Db 77 IVGQCRLDQALVRKRWNSFELLCSKPSKLPMPGFGGKALEWLVDAKTRPESPDFI 131
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTDPITALRDADRVTLGLLECDGIRDKIMVNRVT 238
Db 132 LIDCPAGIDVGFNAISASAQEAIVVTPETIAIRADRVAGLLEANGIYNVKNVLRVP 191
QY 239 DMKICEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 298

Db 192 DMKICEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 251
QY 299 RLV-EQDSMKAYMVEEPPKRGFF-----SFFGQ 326
Db 252 RLTRQD-----VFIDITSPQKMPKLOEFFFLG 280

RESULT 3

MIND_GUITH STANDARD: PRT: 269 AA.
AC 078436;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Guillardia theta (Cryptomonas phi).
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved syntenic groups confirm its common
RT ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC
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CC Or send an email to license@isb-sib.ch).
CC
CC EMBL: AF041468; AAC35621.1;
DR InterPro: IPR000707; Para.
DR Pfam: PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Chloroplast.
FT NP_BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 269 AA: 29455 MW: BC363E954E689EA2 CRC64;

Query Match 42.0%; Score 694.5; DB 1; Length 269;
Best Local Similarity 55.9%; Pred. No. 5.1e-49;
Matches 146; Conservative 44; Mismatches 62; Indels 9; Gaps 3;

QY 59 RIVVITSGKGGVCKTTTANVGLSLARYGSVVAIDAGLRLNLDLLGLNVRVNTQVE 118
Db 3 RVVITSGKGGVCKTTTANVGLSLARYGSVVAIDAGLRLNLDLLGLNVRVNTQVE 62
QY 119 VINGCDRLDQALVRKRWNSFELLCSKPSKLPMPGFGGKALEWLVDAKTRPESPDFI 178
Db 63 VLSGCRLEQALIKRQPNLVLLPAAQNRNK--DSVTEEQMKFLVNL-----VNDYDYL 116
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTDPITALRDADRVTLGLLECDGIRDKIMVNRVT 238
Db 117 LIDCPAGIETGFHNAIGPAQEAIVVTPETIAIRADRVIGLLEANGIKKLVNRLRP 176
QY 239 DMKICEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 298
Db 177 QMVKANDMMSVLDVQEMGLSLGLVIGEDSEVIRSTNRGFFLYLNK 236
QY 299 RLV-EQDSMKAYMVEEPPKRG 319
Db 237 RL---DGQEIEFLDQSYSG 254

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RESULT 4
MIND_SYNY3
ID MIND_SYNY3 STANDARD; PRT; 266 AA.
AC Q55900;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR SLL0289.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Szuka T., Miyajima N.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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DR EMBL; D64005; BAAL0662.1; -.
DR InterPro; IPR000392; NitrogenaseII.
DR InterPro; IPR000707; Para.
DR Pfam; PF00142; fer4_NifH; 1.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Membrane; Complete proteome.
FT NP_BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 266 AA; 29047 MW; 4BC37880F086C9BF CRC64;

Query Match 38.9%; Score 643; DB 1; Length 266;
Best Local Similarity 52.8%; Pred. No. 7.le-45;
Matches 130; Conservative 51; Mismatches 59; Indels 6; Gaps 2;

Qy 59 RIVVTSKGGVGKTTTANVGLSLARYGFSVVAIDADLGLRLNLDLLGLNRYNYTCVE 118
Db 3 RIIVVTSKGGVGKTTTANVGLAARLKGKVVLDADFGRLNLDLLGLNRYNYTAID 62

Qy 119 VINGCDRLDQALVRDKRNSNFELLCISKRSLPMFGGKALEWLVDALKTRPEGSPDTI 178
Db 63 VLADECTIDKALVKDKRLPNLVLPAQRKSK--DAINAEQMSQSLVEQLKDK----FDVI 116

Qy 179 IIDCPAGIDAGFITAITANEAVLVITTPDITRALDRVVTGLLECDGIRDIKMNVRVT 238
Db 117 IIDCPAGTEAGFRNVAFAQEAIIITTPMSAVRDVRIIGLEAEDIGKISLVNRLRP 176

Qy 239 DMKCEDMNSVLVDLMGLSLGLVPEDESVIRNTRGFPPLVLPKPTTLAGLAFQAQAW 298
Db 177 EMVQLNQMSIVEDILDLAVLPIGLIPDDQKIIISTNKGEPVLWEKLSVPGIAFQNIAR 236

Qy 299 RVEQD 304
Db 237 RLEGQD 242
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RESULT 5
MIND_BACSU
ID MIND_BACSU STANDARD; PRT; 268 AA.
AC Q01464;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR DIVIVB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RA Varley A.W., Stewart G.C.;
RT "The divIVB region of the Bacillus subtilis chromosome encodes
RT homologs of Escherichia coli septum placement (minCD) and cell shape
RT (mreBCD) determinants.";
RL J. Bacteriol. 174:6729-6742(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RA Lee S., Price C.W.;
RT "The minCD locus of Bacillus subtilis lacks the minE determinant that
RT provides topological specificity to cell division.";
RL Mol. Microbiol. 7:601-610(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211302; PubMed=8459776;
RA Lee S., Price C.W.;
RT "Identification of Bacillus subtilis genes for septum placement and
RT shape determination.";
RL J. Bacteriol. 174:6717-6728(1992).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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CC -----
DR EMBL; M95582; AAA22609.1; -.
DR EMBL; Z15113; CAA78818.1; -.
DR EMBL; M96343; AAA22401.1; -.
DR EMBL; Z99118; CAB14759.1; -.
DR PIR; S31205; S31205.
DR PIR; G45239; G45239.
DR PIR; F45240; F45240.
DR Subtilist; BG10330; minD.
DR InterPro; IPR000392; NitrogenaseII.
DR InterPro; IPR000707; Para.
DR Pfam; PF00142; fer4_NifH; 1.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Membrane; Complete proteome.
FT NP_BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 268 AA; 29407 MW; 6665E9F693F58A9B CRC64;
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DR EMBL; AE000551; AAD07400.1; -.
DR TIGR; HP0331; -.
DR InterPro; IPR000392; NitrogenaseII.
DR InterPro; IPR000707; Para.
DR Pfam; PF00142; fer4_NLH; 1.
DR Pfam; PF00991; Para; 1.
DR Cell division; septation; ATP-binding; Membrane; Complete proteome.
KW NP_BIND 10 17
FT SEQUENCE 268 AA; 20294 MW; 9E14766BD309476 CRC64;
SO SEQUENCE

Query Match      30.68; Score 506.5; DB 1; Length 268;
Best local similarity 40.1%; Pred. No. 7.4e-34;
Matches 110; Conservative 65; Mismatches 80; Indels 19; Gaps

Qy 60 IWVTSKGGVGKTTTANVGLSLARYGESVALDAGLGRLNLDLLGLNRNYTCYEY 119
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 VVTTSKGGVGKTTTANLAIGLESKKVVAVDFDIGRLNDMLILGLENRIYDVVDV 63

Qy 120 INGCRLDQALVRDKRWSNFELLCISKPRKPLMGFGKALEMLVLDAKTRPEGSPDII 179
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 MEKNCLSQALLTKPKNLSTFLAASQSKNTLDKEKVAI--LINALR---ADFDYL 117

Qy 180 IDCPSGIDACGFIATIPANFAVLVTPDDIPIALRDADRVTGLLEDGIRDTIK----MI 232
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 IDSPAGIESGFHALHADNALVYVTEVSLSURSDRVYGIIDAOKSRAKKGMEVKHLI 177

Qy 233 VNRPVTDWIKCEDMNSVLDVOEMCLGILGVPEDSVIRSTSRFPFLVNKPPTLAGLA 232
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 178 INRKPELVANGEMISIEVLKILCLPILGIIPEDHHSIATNKGPVI--RTDCSAKA 235

Qy 293 FEQAARWLVEQDSMKAYVBEPEKRGRFFSFEGG 326
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 236 YQITRRILGEE-----VEYVEFRAKRGFFSNLKG 265

RESULT 7
MIND_HELPJ
ID MIND_HELPJ STANDARD; PRT; 268 AA.
AC Q9ZMAR;
DP 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SPTOM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR JHP0314.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120537; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.F., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.G., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Urtia-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "genomic sequence comparison of two unrelated isolates of the human
RA gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE PTSE FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH MIND AND FTSZ (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY, MIND SUBFAMILY.
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RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kaihara M., Kanai K., Kashimoto K.,

RA Yamada C., Kizugawa K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Mori I., Molomodu K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.,
RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155(1996).
[4]
RP SEQUENCE OF 1-12.

RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of *Escherichia coli* K-12";
MEDLINE=97433973; PubMed=9298046;

[5] ELECTROPHORESIS 16:1259-1313(1997).
RN
RN
RN
FUNCTION, AND MUTAGENESIS.
RX MEDLINE=92097557; PubMed=1836760;
RX de Boer P.A.J., Crossley R.E., Hand A.R., Rothfield L.I.;
RT "The Mind Protein is a membrane ATPase required for the correct
RA placement of the Escherichia coli division site.";
RL EMBO J. 10:4371-4380(1991).
[6]
RN CHARACTERIZATION.
RP MEDLINE=99238467; PubMed=10220403;
RX Raskin D.M., de Boer P.A.;
RT "Rapid pole-to-pole oscillation of a protein required for directing
RA division to the middle of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:4971-4976(1999).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY

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-!- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED.
-!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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EMBL: J03153; AAB59062.1; -.
EMBL: AF000216; AAC74259.1; -.
EMBL: D90751; BAA36009.1; -.
EMBL: D90752; BAA36022.1; -.
PIR: B31877; CCECID.
SWISS-2DPAGE: P18197; COLI.
Ecogene: EG10597; mind.
InterPro: IPR000707; Para.
Pfam: PF00391; Para; 1.
Cell division; Septation; ATP-binding; Inner membrane;
Complete proteome.
INIT_MET 0 0
NP_BIND 9 16 ATP (POTENTIAL).
MUTAGEN 14 14 G->S: LESS EFFECTIVE THEN WILD-TYPE.
MUTAGEN 15 15 K->Q: LOSS OF ACTIVITY.
MUTAGEN 15 16 KT->QR: LOSS OF ACTIVITY.
SEQUENCE 269 AA; 29483 MW; 0D1E29A476A190B1 CRC64;
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Query Match 29.0%; Score 479; DB 1; Length 269;
Best Local Similarity 39.9%; Pred. No. 1.2e-31;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

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SQ SEQUENCE 269 AA; 29805 MW; 4FFD5764549C8B27 CRC64;

Query Match 27.8%; Score 460; DB 1; Length 269;
Best Local Similarity 38.3%; Pred. No. 4.2e-30;
Matches 106; Conservative 60; Mismatches 91; Indels 20; Gaps 5;

Qy 59 RIVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDADLGLRNLDDLGLLENRVNVTCTVEI 118
Db 2 RIIVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDADLGLRNLDDLGLLENRVNVTCTVEI 61
Qy 119 VINGDCRLDQALVRDKRNSNFELLCISPRSKLPMGFG--KALEWLVDAKTRREGSPD 176
Db 62 VIQGDATLNOAIIKDKTNLNFILPASQTRDKDALTRIGCVKLTSLI-----KMNFD 114
Qy 177 FIIDCPAGIDAGFTAITPANEAVLVTPDITLRDADRVTLGLCEGDGIRDK----- 230
Db 115 FLICDSPAGIEGAILAIFYADEAITTNPEVSSVRDSDRIILGISSKSKRAEKNIPTIK 174
Qy 231 --MIYNRVTDIMKGEDMMSVLVDQEMGLSLGVLIPEDSEVIRSTNRGFPVLVKNKPPTL 288
Db 175 EYLLLTRYNPRVKGEMLSMTDVLDIQIPIIGVIPPEDQSVLRASNOGESIILINSN- 233
Qy 289 AGLAPEQAARLVQDSMKAVMVEEPEPKRGEFSFFG 325
Db 234 AGCAYSDTVNRLGEE--RHFRFIEERKSKFLRLRFG 268

RESULT 11
Y547_METJA STANDARD; PRT; 264 AA.
AC Q57967;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL ATP-BINDING PROTEIN MJ0547.
GN MJ0547.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RT Science 273:1058-1073(1996).
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: HIGH, TO M.JANNASCHII MJ0169 AND MJ0410.
CC -!- SIMILARITY: SOME, TO PROKARYOTIC MIND AND TO THE MRP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67504; AAB98539.1; -
CC TIGR; MJ0547; -
CC InterPro; IPR000392; NitrogenaseII.
CC DR PFam; PF00142; fer4_NifH; 1.
CC DR PFam; PF00991; Para; 1.
CC DR
```

```
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 13 21 ATP (POTENTIAL).
SQ SEQUENCE 264 AA; 27737 MW; B9AF5108CDD0CEC3 CRC64;

Query Match 18.1%; Score 300; DB 1; Length 264;
Best Local Similarity 30.5%; Pred. No. 3.3e-17;
Matches 82; Conservative 57; Mismatches 104; Indels 26; Gaps 6;

Qy 61 VVITSGKGGVGTNTTANVGLSLARYGFSVVAIDADLGLRNLDDLGLLENRVNVTCTVEI 120
Db 9 IAIASGKGVTGKTTISANLAVAKFGKVAVLDADTAMANLELIMGLEK-----PVT 62
Qy 121 NGDCRLDQALVRDKRNSNFELLCISPRSKLPMG-----FGKALEWLVDAKTRREGSP 175
Db 63 LNDVLGAKADIKDAIVEGPGVLV-----IPAGVLEKERRAKPEKLEEVKLAHD-LV 115
Qy 176 DFIIDCPAGIDAGFTAITPANEAVLVTPDITLRDADRVTLGLCEGDGIRDKIMVNR 235
Db 116 EILIIDCPAGIGKETLIAISSADGLIVVNPETISSIDALKIIAITKRLGTDIIGAIVNR 175
Qy 236 VRTDMIKGEDMMSVLVDQEMGLSLGVLIPEDSEVIRSTNRGFPVLVKNKPPTLAGLAF 295
Db 176 VSNESTE---LGVKAETILEVPVIGVVPEDPHVRKAAAFGLVIMYPDSPAAQAI 231
Qy 296 AAWRLVEQDSMKAVMVEEPEPKRGEFSFF 324
Db 232 IAAKLLG-----AKYEAQLKKKESFISKF 256

RESULT 12
Y169_METJA STANDARD; PRT; 263 AA.
AC Q57633;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL ATP-BINDING PROTEIN MJ0169.
GN MJ0169.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RT Science 273:1058-1073(1996).
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: HIGH, TO M.JANNASCHII MJ0547. SOME, TO MJ0410 AND
CC TO MJ0924.
CC -!- SIMILARITY: SOME, TO PROKARYOTIC MIND AND TO THE MRP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67474; AAB98154.1; -
CC TIGR; MJ0169; -
CC InterPro; IPR000392; NitrogenaseII.
CC DR
```



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DR InterPro: IPR000707; ParaA.  
DR Pfam: PF00142; fer4_NiH; 1.  
DR Pfam: PF00991; Para; 1.  
KW Hypothetical protein; ATP-binding; Complete proteome.  
FT NP_BIND 10 17 ATP (POTENTIAL).  
SQ SEQUENCE 263 AA; 28950 MW; 292FDE30EE72AG4 CRC64;  
  
Query Match 14.6%; Score 242; DB 1; Length 263;  
Best Local Similarity 29.3%; Pred. NO. 1.6e-12;  
Matches 77; Conservative 59; Mismatches 99; Indels 28; Gaps 9;  
  
QY 60 IIVITSGGGVKTITANVGLSLARYGFSVVAIDADLGLRNLDDLGLLENRYNTVEY 119  
Db 5 IITIASGGVGGKTTTASLAVALKKKVLAIDGDSMANLGLFNKKR-KPSLHEV 63  
QY 120 INDCRLDQALVRD---KRWNFPELLQTSKPSKSLPMGFGKALEWLVDALKTRPEGSPD 176  
Db 64 LS-----EADVRDAIYKHTGVVVL-----PTSLSEYKKSDIDLLDFVYNEVADDF-D 113  
QY 177 FIIDCPAGIDAGFITATPANEAVALVTPDITARDADRVTLGECGIRDKIMVNRV 236  
Db 114 VVIIDADAGLRNEMATHAIADKLLLVTPPEMFISIIDAVRLKESAEAGTPLMGVVLNRV 173  
QY 237 RTDMIKGEDMNSVLDVQEMLSLLGVIPEDSEVIRSNRGPFLY---LNKPEPTLAGLAF 293  
Db 174 GRDF--GE--NGRDEIMLIGKVLVEPDEDENVRSAALKMNSVIEYRKNSPAS----- 223  
QY 294 EQAAWRLVEODSMKAVMVEEPK 316  
Db 224 QATYKKLASIIAGVPIEDRIK 245  
  
RESULT 13  
YLXH_BACSU STANDARD; PRP; 298 AA.  
AC P40742; 1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL 33.2 KDA PROTEIN IN FLHF-CHEB INTERGENIC REGION (ORF298).  
GN YLXH.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI_TaxID=1423;  
RN [1]  
RD SEQUENCE FROM N.A.  
RX MEDLINE=95078462; PubMed=7987014;  
RA Kirsch M.L., Carpenter P.B., Ordal G.W.;  
RT "A putative ATP-binding protein from the che/fla locus of Bacillus  
subtilis.";  
RL DNA Seq. 4:271-275(1994).  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: X73682; CAA52034.1; -  
DR EMBL: 299112; CAB13514.1; -  
DR PIR: S34194; S34194.1; YLXH.  
DR Subtilist; HG10254; ylxH.  
DR InterPro: IPR000392; NitrogenaseI1.  
DR InterPro: IPR000707; ParaA.  
DR Pfam: PF00142; fer4_NiH; 1.  
DR Pfam: PF00991; Para; 1.  
KW Hypothetical protein; ATP-binding; Complete proteome.  
FT NP_BIND 39 46 ATP (POTENTIAL).  
SQ SEQUENCE 298 AA; 33160 MW; AF6FE71FA3C1C972 CRC64;  
  
Query Match 12.9%; Score 214; DB 1; Length 298;  
Best Local Similarity 25.2%; Pred. No. 3.3e-10;  
Matches 76; Conservative 56; Mismatches 119; Indels 50; Gaps 10;  
  
QY 32 YNPNRSRPIRSYLQENRK--PELAGETPRIVVITSGGKGVGKTTTANVGLSLARVQPS 89  
Db 3 MARYDOAAFLRAKMEKRERVLPMVYSOKAKTLAVISGGKGVGKSNITLNMALADOKGKK 62  
QY 90 VVAIDADLGLRNLDDLGLLENRYNTVEYINGDCRLDQALYDRKRWNSFELLCLCKSPRS 149  
Db 63 VLLIDLTGMDIDILG--NSSATIIDVLRKPLLOS-----S 102  
QY 150 KLPMGF---GGKALE-----WLVDALKTRPESP-DFIIDCPAGIDAGFITAT 193  
Db 103 YGPKGLRYISGGTGLDVMFQDQRKWTFFANELSHALSQFDVYLFDMGAGLSKQDLQPFIL 162  
QY 196 PANEAVLVTPDITARDADRVTLGECGIRDKIMVNRVTPDMIKGEDMNS----- 248  
Db 163 SAEDILIIITPEPTAIMDAISAVKHLVLTENKLSMKVAVNRCK-DQKEGLDAFARLSRTI 221  
QY 249 --VLDVQEMLSLLGVIPEDSEVIRSNRGPFLVNLNKPPTLACLAFAEAAVRLVQDSM 306  
Db 222 HMFIDVO-----VOPAGSVGDDVIVSKAVVEOVFFFKSPQAKASRSVRILADALFERET 277  
QY 307 K 307  
Db 278 R 278  
  
RESULT 14  
MRP_SYNY3 STANDARD; PRT; 353 AA.  
AC P53383;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE MRP PROTEIN HOMOLOG.  
GN MRP OR SLR0067.  
OS Synecocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
OX NCBI_TaxID=1148;  
RN [1]  
RD SEQUENCE FROM N.A.  
RX MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
RA Suglura M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
region from map positions 64% to 92% of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -!- FUNCTION: NOT KNOWN.  
CC -!- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING  
CC PROTEINS.  
CC -----  
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CC -----  
CC EMBL: D64001; BAA10297.1; -  
DR InterPro: IPR002744; DUF59.  
DR InterPro: IPR000808; MRP.  
DR InterPro: IPR000392; NitrogenaseI1.  
DR Pfam: PF01883; DUF59; 1.  
DR Pfam: PF00142; fer4_NiH; 1.  
DR Pfam: PF00142; fer4_NiH; 1.  
DR ProbDom: PD005595; DUF59; 1.  
DR PROSITE: PS01215; MRP; 1.  
KW ATP-binding; Complete proteome.
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FT NP_BIND 105 112 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 37131 MW; 891DC0E247113841 CRC64;

Query Match 12.9%; Score 213; DB 1; Length 353;
Best Local Similarity 26.1%; Pred. No. 5e-10;
Matches 82; Conservative 55; Mismatches 115; Indels 62; Gaps 12;

QY 23 KTLISPRFVNPPSRPSIRSVLQFNKRPKELAGETPRIVVITSGKGGVGGKTTTANVGLS 82

DB 76 KYTAETPOOKSLPDRQS-----VGQVKNIIAISGKGGVGGKSVAVNVAVA 121

QY 83 LARYGSFVVAIDADGLRLNLDLLGLLENRVNYTCVEVINGDCRLDQALVRDKWSNFELL 142

DB 122 LAQTGAAGVLLDADYGNAPTMLGLSG---AAVQVQNS---PQGEVLEPVF-NHGK 172

QY 143 CISKPSKLPKMGF-----GGKALEWLVDAKTRPE-CSPDFIIIDCPAGI-DAGF 190

DB 173 MVS-----MGFLIDPDQPVIVRGPMPLNGIIRQFLYQVNWGALDYLVDMPPGTGDAQL 225

QY 191 -ITAITPANEAVLVTPDITALRDVVTGLLECDGIRDIKMIVNR---VRTDMK--- 242

DB 226 TLTQSVPHAGAVITPQTIVSLDARRGLKMFQMGVNVGIVENMSYFIPDPLDRQYD 285

QY 243 -----GEDMMSVLDVQEMLGLSLGVIPEDSEVIRSTNRGFPVLVKNKPTTLAGLAF 296

DB 286 LFGSGGGEKASKELNV-----PLLCGVPLEIGLREGGDKGVPIVVSQPEASAKALTAI 339

QY 297 AWRLVEQDSMKRAVM 310

DB 340 AKQIAGKVSMALV 353

RESULT 15

MRP_AQUAE

ID MRP_AQUAE STANDARD; PRT; 364 AA.
AC O66946;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE MRP PROTEIN HOMOLOG.
GN MRP OR AQ_737.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING
CC PROTEINS.

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DR EMBL: AE000705; AAC06915.1; -
DR InterPro: IPR000808; MRP.
DR InterPro: IPR000392; NitrogenaseII.
DR Pfam: PF00142; fer4_NiH; 1.
DR PROSITE: PS01215; MRP; 1.
KW ATP-binding; Complete proteome.

FT NP_BIND 120 127 ATP (POTENTIAL).
SQ SEQUENCE 364 AA; 39492 MW; 320AF95C191A272A CRC64;

Query Match 12.8%; Score 211; DB 1; Length 364;
Best Local Similarity 27.1%; Pred. No. 7.5e-10;
Matches 75; Conservative 50; Mismatches 110; Indels 42; Gaps 10;

QY 35 PSRRSPISRVLQFNKRPKELAGETPRIVVITSGKGGVGGKTTTANVGLSILARYGFSVVAID 94

DB 96 PQTQOPM-----FTRK-KVPG-VKHITAVGSGKGGVGGKSTVAANLAVALSQGLYKVGVLID 148

QY 95 ADGLRLNLDLLGLLENRVNYTCVEVINGDCRLDQALVRDKWSNFELLCISKPRSKLPMG 154

DB 149 ADVYGPSVPTLFGKLG-----ERVTVD-QFRIIPVEKYGLKILSIGFMPLPSEDTPII 200

QY 155 FGGKAL-EWLVDALKTRPEGSPDFIIIDCPAGIDAGFTAI--TPANEAVLVTTPTDITAL 211

DB 201 WRGPMMLKALTEFLSTKGNLDELVDLPPTGVDVQITLAQNVELTGAVVVVTTPODVAL 260

QY 212 RDADRVVTGLLECDGIRDIKMIVNRVTDMI-----KGEDMMSVLDVQEML 256

DB 261 ADVKKAVSM-----FREVNIPLVGLVIENMAYFICPSDKOKYIFGKGR-----VAEFANAY 311

QY 257 GLSLGVIPEDSEVIRSTNRGFPVLVKNKPTTLAGLAF 293

DB 312 GLKILGISIPIDPEVAEKSDKGEPIVISHPDSEVAKAF 348

Search completed: February 11, 2002, 13:33:23
Job time: 125 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 16.09 Seconds
(without alignments)
1543.375 Million cell updates/sec

Title: US-09-553-431-2

Perfect score: 1654

Sequence: 1 MASLRLFTNHQSLLLPSSL.....KAVNVEEPPKRGFFSFFGG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	47.9	282	T07303	cell division inhi
2	643	38.9	266	S76970	hypothetical prote
3	573.5	34.7	276	D75478	septum site-determ
4	536.5	32.4	264	C84028	septum site-determ
5	523	31.6	268	G45239	cell division inhi
6	516	31.2	262	F70375	cell division inhi
7	514.5	31.1	269	C82695	septum site-determ
8	506.5	30.6	268	C64561	cell division inhi
9	500.5	30.3	268	B71945	cell division inhi
10	480.5	29.1	271	F83239	cell division inhi
11	479	29.0	270	CECID	cell division inhi
12	479	29.0	270	F85695	hypothetical prote
13	475.5	28.7	271	A72200	septum site-determ
14	468	28.3	276	C82136	septum site-determ
15	460	27.8	270	B84968	septum site-determ
16	449.5	27.2	271	C81230	septum site-determ
17	366	22.1	260	F75175	cell division inhi
18	344.5	20.8	259	B59113	cell division inhi
19	341.5	20.6	245	C71105	probable cell divi
20	335	20.3	263	H69336	cell division inhi
21	327.5	19.8	245	A75056	cell division inhi
22	300	18.1	264	C64368	cell division inhi
23	266	16.1	252	F71191	hypothetical prote
24	262.5	15.9	305	A84363	cell division inhi
25	254	15.4	217	H71038	probable cell divi
26	249	15.1	280	B83463	flagellar synthesi
27	247.5	15.0	251	H75150	cell division inhi
28	246.5	14.9	288	D83954	hypothetical prote
29	243.5	14.7	323	B84251	cell division inhi

30	242	14.6	263	1	B64321	cell division inhi
31	241	14.6	288	2	C81422	probable ATP-bindi
32	239.5	14.5	304	2	D71290	probable ATP-bindi
33	238.5	14.4	295	2	E70133	ATP-binding protei
34	230	13.9	294	2	B64649	ATP-binding protei
35	228	13.8	313	2	B82123	MinD-related prote
36	224	13.5	294	2	D71938	hypothetical prote
37	214	12.9	298	2	I40434	flagellar biosynth
38	213	12.9	353	2	S74379	probable ATPase -
39	211	12.8	364	2	G70364	conserved hypothet
40	209.5	12.7	378	2	E71274	probable ATP-bindi
41	209	12.6	368	2	H71962	hypothetical prote
42	206	12.5	412	2	G64545	ATP-binding protei
43	204.5	12.4	278	2	H70404	cell division inhi
44	202	12.2	297	2	H75132	hypothetical prote
45	197.5	11.9	350	2	F75448	mrp protein - Dein

ALIGNMENTS

RESULT 1

T07303

cell division inhibitor - Chlorella vulgaris chloroplast

C:Species: chloroplast Chlorella vulgaris

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C:Accession: T07303

R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na
proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga C

A:Reference number: Z15985; MUID:97303241

A:Accession: T07303

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-282 <WAK>

A:Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57951.1; PID:g2224467

C:Genetics:

A:Gene: mind

A:Genome: chloroplast

C:Superfamily: cell division inhibitor mind

C:Keywords: chloroplast

Query Match 47.9%; Score 792; DB 2; Length 282;
Best Local Similarity 60.4%; Pred. No. 4.6e-56;
Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

Qy 59 RIVVITSGKGVGKTTTANVGLSIARYGFSVVAIDADGLRLNLDLLGLNRYNYTCVE 118

Db 17 RVIVITSGKGVGKTTTANGLMSIARLGYRVALIDADIGLRNLDLLGLNRYLYTAMD 76

Qy 119 VINGDCRLDQALVRDRKWSNFELLCISKRSLKPMFGFGKALEWLVDAKTRPEGSPDFI 178

Db 77 IVEGQCRLDQALIRDRKWNKLLALLAISKNROK--YNYTRKNQNLIDSVK---ELGFOFV 131

Qy 179 IIDCPAGIDAGFITAITPANEAVLVTPTDIPALRDADRVTLGLEDGIRDKIMVNRVRT 238

Db 132 LIDCPAGIDVGFINAIASAQEAIVTTPETIARDADRVAGLLEANGIYVKNLLVNRVRP 191

Qy 239 DMKGEDMMSVLDVQEMLGSLGLGVIPEDSEVIRSTNKGFPPLVNLKPPFLAGLAEQAAW 298

Db 192 DMIOKNDMSVRDQVQEMLGIPFLGAIPEDTSVIITNKGFLVNLKLTLSGIAFENAR 251

Qy 299 RLV-EQDSMRKAVMVEEPPKRGFF----SFFGG 326

Db 252 RLIGKQD-----YFDLITSPQKMFQKLOEFFLG 280

RESULT 2

S76970

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

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119 QY VINGCDRLDOALVRKRWSNFELLCSIKPRSKLPMGFGGKALEWLDALKTR----- 170
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
72 DB VLESGKCRMNQALLRDKRVENLHLLPASQTRDK-----DALDPEVKEVKVG 117
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

171 QY --DEGSPDFTIIDCPACIDAGFTATTPANEAVLVTPTDITALURDADRVYTGLEECGIRD 328
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
118 DB LLEFEGFDRVLIDSPAGIESGFRTAAPAGALVVVNPEVSSVRDADRIIGLLEAQOITE 177
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

229 QY IKMIVNRFRDMTIKGDMMSVLVDVQEMGLSLGVLGVPIDSEVIRSTNRGFPVLVKNPPTL 288
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
178 DB IRLVNLRLPKWASGNMLSIDMDWDILGVKPGICVPEDEGITVSTNVGEPAVLGR--TK 235
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

289 QY AGLAFQCAAWRLVEQDSMKAVWVEEPPKRGFFS----FFGG 326
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
236 DB AGDAFNATAGRIQGVDPVPPKLTTEE---KGIWAAILRRLFFGG 274
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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RESULT 4
C84028
septum site-determining protein minD [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: C84028
R:R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H.
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: C84028
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06746.1; GSPDB:G-
A:Experimental source: strain C-125

Query Match 32.4%; Score 536.5; DB 2; Length 264;
Best Local Similarity 41.1%; Pred. No. 1.2e-35;
Matches 109; Conservative 56; Mismatches 83; Indels 7; Gaps 3;
QY 61 VVLTSGKGGVGKTTTANYGLSLARYGFSVYADADLGLRNLDLLGLLENRYNYTCVEVI 120

[illegible]

cell division inhibitor mind [validated] - Bacillus subtilis
N: Alternate names: septum placement determinant mind
S: Species: Bacillus subtilis
C: Date: 10-Jun-1993 #sequence_revision 04-Oct-1996 #text_change 0
C: Accession: S31203; G45239; F45240; A69658; S27521; S29866
R: Price, S.; Price, C.W.
Mol. Microbiol. 7, 601-610, 1993

[illegible]

A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Doiry, H.; Facincani, A.P.; Ferreira, A.J.S. Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A5328
A:Contents: annotation
C:Genetics:
A:Gene: XFI321
C:Superfamily: cell division inhibitor mind

Query Match 31.1%; Score 514.5; DB 2; Length 269;
Best Local Similarity 43.5%; Pred. No. 7.1e-34;
Matches 120; Conservative 56; Mismatches 79; Indels 19; Gaps 8;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 119
Db 4 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 63
QY 120 INDCRLDQALVDRKWSNFELLCISKPSKLPFGGKALEWLDALKTRPEGSPDFII 179
Db 64 IDENTLKQALIKRDNLYLLAAOTRDKALTKEG--VEKVLNELQA--EGP-DYIC 118
QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGL-----ECGINDIKMI 232
Db 119 CDSFAGTEKASLAMYADRAVYVNVVPEVSSVRSDRIIGLDSKTKAETGGSTITLL 178
QY 233 VNRVRTDMIKEDMMSVLDVQEMGLSLGVLTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292
Db 179 LTRYSPARVESGEMLSIADVEVLGLKAIGVIPSQGVLDNLSNKGPEVILDN-NSLAGIA 237
QY 293 FEQAARLVLEQD-SMKAVMYVEEPEKRGFFS-FFGG 326
Db 238 YEDAVGRILGEDHPMRITVE----KKGFFSKLFGG 269

RESULT 8
C64561
cell division inhibitor mind - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 02-Feb-2001
C:Accession: C64561
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A:Reference number: A64520; MUID:97394467
A:Accession: C64561
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-268 <TOM>
A:Cross-references: GB:AE000551; NID:g2313430; PIDN:AAD07400.1; PID:g231343
C:Genetics:
A:Gene: mind
C:Function:
A:Description: an ATPase required for correct placement of cell division site
C:Superfamily: cell division inhibitor mind
C:Keywords: ATP; cell division control; nucleotide binding; P-loop
F:10-17/Region: nucleotide-binding motif A (P-loop)
F:16/Binding site: ATP (Lys) #status predicted

Query Match 30.6%; Score 506.5; DB 2; Length 268;
Best Local Similarity 40.1%; Pred. No. 3.1e-33;
Matches 110; Conservative 65; Mismatches 80; Indels 19; Gaps 5;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 119
Db 4 VVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 63
QY 120 INDCRLDQALVDRKWSNFELLCISKPSKLPFGGKALEWLDALKTRPEGSPDFII 179
Db 64 MEKNCNLSQLITDKTKNLSFLAASQSKDNLDKRVAI--LINALR----ADPDYIL 117
QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGLLECDGIRIK-----MI 232
Db 118 IDSPAGIESGFHAHLHADMALVYVVTPEVSSLRSDSVYGIIDAKSNRAKKGVEVHKHII 177
QY 233 VNRVRTDMIKEDMMSVLDVQEMGLSLGVLTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292
Db 178 INRLKPELVANGEMISIEVLKILCLPLIGIIPEDHIIISATNKGEPI--RTDCESAKA 235
QY 293 FEQAARLVLEQD-SMKAVMYVEEPEKRGFFS-FFGG 326
Db 236 YORITRRLIGEE---VEYVEFKARGPFSALKG 265

RESULT 9
B71945
cell division inhibitor - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 26-Aug-1999
C:Accession: B71945
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D. Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A:Reference number: A71800; MUID:99120557
A:Accession: B71945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <ARN>
A:Cross-references: GB:AE001469; NID:g4154938; PIDN:AAD05905.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: mind
C:Superfamily: cell division inhibitor mind

Query Match 30.3%; Score 500.5; DB 2; Length 268;
Best Local Similarity 39.8%; Pred. No. 9.3e-33;
Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 119
Db 4 VVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLGLLENRVNVTCEV 63
QY 120 INDCRLDQALVDRKWSNFELLCISKPSKLPFGGKALEWLDALKTRPEGSPDFII 179
Db 64 MEKNCNLSQLITDKTKNLSFLAASQSKDNLDKRVAI--LINALR----ADPDYIL 117
QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGLLECDGIR-----DIKMI 232
Db 118 IDSPAGIESGFHAHLHADMALVYVVTPEVSSLRSDSVYGIIDAKSNRAKKGVEVHKHII 177
QY 233 VNRVRTDMIKEDMMSVLDVQEMGLSLGVLTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292
Db 178 INRLKPELVANGEMISIEVLKILCLPLIGIIPEDHIIISATNKGEPI--RTDCESAKA 235
QY 293 FEQAARLVLEQD-SMKAVMYVEEPEKRGFFS-FFGG 326
Db 236 YORITRRLIGEE---VEYVEFKARGPFSALKG 265

Db 63 VIQDATLNQALIKDKRTENLYILPASQTRDKDALTREGVAK--VLDDLKAM--DFEFI 117

QY 179 IIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC-----DCIRDIK-- 230
Db 118 VCDSPAGIETGALMAYFADEAIITNPEVSSVSDRSLDGLTLAKSKSRRAENGEEPIKEH 177
QY 231 MIYNVRVTDMKIGEDMMSYLDVQEMGLSLGVLGVPEDSEVIRSTNRGFPVLNKPETLAG 290
Db 178 LLLTFYPCVRSGDMSLWEDVLEILTKVLGVIPEDQSVLQASNOGEPVILDINAD-AC 236
QY 291 LAFOQAAWRLVEQDSMKVAMVVEEP-----KKRGFFS-FFGG 326
Db 237 KAY-----ADTVRLGGBERFPEIEBKGFLLKRLFGG 270

RESULT 13
A72200
septum site-determining protein mind - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: A72200
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <ARN>
A:CROSS-references: GB:AE001824; GB:AE000512; NID:94982455; PIDN:AAD36932.1; PID:9498245
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1870
C:Superfamily: cell division inhibitor mind

Query Match 28.7%; Score 475.5; DB 2; Length 271;
Best Local Similarity 40.9%; Pred. No. 9.5e-31;
Matches 105; Conservative 47; Mismatches 68; Indels 37; Gaps 5;

QY 60 IWVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVEV 119
Db 4 VIVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVEV 63
QY 120 INGCRLDOALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLDALKTRPEGSDFI 175
Db 64 VNGKVSQVQALVKHMLKNLYL-----PASQ-----IATKEMISFNDMK 103
QY 176 -----DFIIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 225
Db 104 ATVKELIPFDYIITDPSAGIERGFRNAPAEERVLVVTTPDITARDADRVGTGILEC 163
QY 226 IRD--IKMIVNRVTDMKIGEDMMSYLDVQEMGLSLGVLGVPEDSEVIRSTNRGFPVLN 283
Db 164 FSDEKINVIINRKHMKVKGEMLTDDIKHTLSLEITAVIPDSEDIIVASNTGIPVSLN 223
QY 284 KPPTLAGLAFOQAAWRL 300
Db 224 GNSRIS-KNFENLARRI 239

RESULT 14
C82136
septum site-determining protein mind vc1960 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82136
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B.
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833

A:Accession: C82136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <HEI>
A:CROSS-references: GB:AE004271; GB:AE003852; NID:9656490; PIDN:AAF95108.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1960
A:Map position: 1
C:Superfamily: cell division inhibitor mind

Query Match 28.3%; Score 468; DB 2; Length 276;
Best Local Similarity 40.4%; Pred. No. 3.9e-30;
Matches 112; Conservative 57; Mismatches 90; Indels 18; Gaps 7;

QY 59 RIIVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVE 118
Db 9 RIIVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVE 68
QY 119 VINGCRLDOALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLDALKTRPEGSDFI 178
Db 69 VINGEATLQAALIKDKKNENLFLPASQTRDKDALTQD--YQVLENDLK---EMGFDFI 123
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 230
Db 124 ICDSPAGIEGALMALVYADEAIVTTNPEVSSVSDRSLDGLTLAKSKSRRAENGEEPIKEH 183
QY 231 MIYNVRVTDMKIGEDMMSYLDVQEMGLSLGVLGVPEDSEVIRSTNRGFPVLNKPETLAG 290
Db 184 LILTRNPARVTCQEMLSVQDVEEILHVLLGVIPESQAVLNASKGVPIFDQSD-AC 242
QY 291 LAFOQAAWRLV-EQDSMKVAMVVEEPKKRGFFSFFGG 326
Db 243 QAYQDTVARLIGEQVEFREL---TEAKGIFKRLFGG 276

RESULT 15
B84968
septum site-determining protein mind [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: B84968
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A:Reference number: A84930; MUID:20445173
A:Accession: B84968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <STO>
A:CROSS-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: mind; BU326
C:Superfamily: cell division inhibitor mind

Query Match 27.8%; Score 460; DB 2; Length 270;
Best Local Similarity 38.3%; Pred. No. 1.6e-29;
Matches 106; Conservative 60; Mismatches 91; Indels 20; Gaps 5;

QY 59 RIIVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVE 118
Db 3 RIIVITSGGGVGKTTTANVGLSLARYGSFVVAIDADLGLRLNLDLLGLLENRVNVTCTVE 62
QY 119 VINGCRLDOALVRDKRWSNFELLCISKPRSKLPMGFGG--KALEWLDALKTRPEGSDF 176
Db 63 VIQDQATLQAALIKDKKNENLFLPASQTRDKDALTGRIGVKVLTETI-----KMFED 115
QY 177 FIIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 230
Db 116 FIIDCPAGIETGALMALVYADEAIVTTNPEVSSVSDRSLDGLTLAKSKSRRAENGEEPIKEH 175

QY 231 --MIVNRVRTMIKEDMMSVLDVQEMLGSLGLGVTPEDSEVIRSTNRGFPPLVLNKPPTL 288
Db 176 EYLLLTRYNPRRVKKGEMLSMTDVLQIPITGVIPEDQSVLRASNOGESIILDINSN - 234
QY 289 AGLAFEAQAAWRLVEQDSMKAVWVEEPKKRGFSFPG 325
Db 235 ACAYSDTVNRLGEE--RHFRFIEEEKKSFLRRFG 269

Search completed: February 11, 2002, 13:33:03
Job time: 110 sec